In the Specification:

Please amend the Specification as follows:

Please replace the paragraph beginning on page 5, line 26, through page 5, line 31 with the following paragraph:

--In a further preferred form the promoter comprises or consists essentially of the construct designated hProm505 being a sequence of nucleotides of 505 bp in length from position ~~-463~~ -436 as shown in Fig. 4 or the construct designated hProm867 being 867 bp in length from position -798 bp (Fig. 4a and Fig. 5a).--

Please replace the paragraph beginning on page 34, line 26 through page 35, line 27 with the following paragraph:

--The present inventors have previously reported the identification of genomic clones in P1 vectors containing hTR and *terc* transcribed sequences~~,~~ (Soder *et al.*, 1997b; Soder *et al.*, 1997c). The human P1 clone, 9913, is derived fron a human foreskin fibroblast P1 library and the mouse P1 clone, 11792, is derived from a mouse C127 fibroblast P1 library. Briefly, in order to subclone the promoter regions, the P1 clones were digested with *Eco*RI and *Hind*III and ligated into pBluscript. Colonies containing telomerase RNA gene sequences were identified by hybridisation with PCR generated probes as previously described~~,~~ (Soder *et al.*, 1997b; Soder *et al.*, 1997c). Plasmid DNA was prepared from positively hybridising colonies, and inserts sequenced on both strands by dideoxy chain termination using the ABI PRISM dye terminator cycle sequencing kit (PE Applied Biosystems, Warrington, UK) and 25ng oligonucleotide primers, Dye labelled products were resolved and detected using the Applied Biosystems DNA sequencer ABI373. Sequence was analysed using the Sequencing Analysis program 3.0. Homology searches were carried out using BLAST~~,~~ (Basic Local Alignment Search Tool), National Centre for Biotechnology Information~~,~~ (NCBI)~~: http://www.ncbi.nlm.nih.gov/~~. Sequence was analysed for potential transcription factor binding sites by TESS: Transcription Element Search

Software on the WWW, Jonathan Schug and G. Christian Overton, Technical Report CBIL-TR-1997-1001-v0.0, of the Computational Biology and Informatics Laboratory, School of Medicine, University of Pennsylvania~~, 1997,~~ ~~http://agave.humgen.upenn.edu/tess/index.html~~. Identification of CpG islands was carried out using GRAIL: Gene Recognition and Assembly Internet Link, ~~http://compbio.ornl.gov/Grail-1.3/~~ Computational Biology Section of the Life Science Division, Oak Ridge National Laboratory. The full sequences have been submitted to GenBank.

Please replace the paragraph beginning on page 44, line 31 through page 45, line 19 with the following paragraph:

--Human promoter constructs containing truncated portions of the 5'-flanking region were transiently transfected into HeLa and GM847 cells, (Figure 5a). HeLa is a telomerase positive cervical carcinoma cell line, GM847 is a SV40-immortalised skin fibroblast cell line which expresses the telomerase RNA component but is telomerase-negative, (Bryan *et al.*, 1997). As shown in Figure 5a, promoter activity was observed in both cell lines with fragments containing 341bp or more, (from position -272, see Figure 4a, 5a). The highest luciferase activity was observed with construct hProm505 which contains a 505bp fragment, (position ~~-463~~ -436, see Figure 4). Construct~~,~~ hProm111, which contains only 111bp of 5'-flanking sequence~~,~~ (position -42 see Figure 4a, 5a), produced a dramatically reduced level of luciferase activity~~,~~ (Figure 5a). Thus a minimal promoter sequence can be defined as extending 272bp upstream of the transcription start site, and that elements responsible for promoter activity must be contained in a 231bp region between -272bp and -42bp~~,~~ (Figures 4a and 5a).--

Following page 76 of the Specification, please insert the attached sheet, page 77. The attached sheet includes an Abstract of Disclosure as required by 37 CFR § 1.72(b)

Attachment: Sheet including Abstract of Disclosure